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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/480,236DATE: 02/01/2000
TIME: 11:11:05

Input Set: I480236.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

<110> APPLICANT: Digan, Mary Ellen
Lake, Philip
Wright, Richard M.
<120> TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
<130> FILE REFERENCE: CGC 4-31157A/USN
<140> CURRENT APPLICATION NUMBER: US/09/480,236
<141> CURRENT FILING DATE: 2000-01-10
<160> NUMBER OF SEQ ID NOS: 22
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO 1
<211> LENGTH: 601
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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20 25 30
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35 40 45
Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Lys Phe
50 55 60
Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu
65 70 75 80
Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
85 90 95
Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly
100 105 110
Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu
115 120 125
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
130 135 140
Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr
145 150 155 160
Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met Gly
165 170 175
Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys
180 185 190
Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
195 200 205
Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala

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46 Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly
47 225          230          235          240
48 Ala Gly Thr Thr Val Thr Val Ser Ser Lys Ala Ser Gly Gly Pro Glu
49          245          250          255
50 Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro
51          260          265          270
52 Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu
53          275          280          285
54 Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
55          290          295          300
56 Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
57 305          310          315          320
58 Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
59          325          330          335
60 Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
61          340          345          350
62 Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn
63          355          360          365
64 Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr
65          370          375          380
66 Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg
67 385          390          395          400
68 Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln
69          405          410          415
70 Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu
71          420          425          430
72 Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln
73          435          440          445
74 Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala
75          450          455          460
76 Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg
77 465          470          475          480
78 Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu
79          485          490          495
80 Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala
81          500          505          510
82 Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp
83          515          520          525
84 Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu
85          530          535          540
86 Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro
87 545          550          555          560
88 Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro
89          565          570          575
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92 Gly Lys Pro Pro Arg Glu Asp Leu Lys
93          595          600
94 <210> SEQ ID NO 2

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96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence:
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103 <222> LOCATION: (1)..(6)
104 <223> OTHER INFORMATION: NcoI restriction site
105 <220> FEATURE:
106 <221> NAME/KEY: misc_feature
107 <222> LOCATION: (336)..(383)
108 <223> OTHER INFORMATION: linker
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (751)..(756)
112 <223> OTHER INFORMATION: HindIII restriction site
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115     gtcaccatca gttgcagggc aagtcaggac attagaaatt atttaaactg gtatcaacag 120
116     aaaccagatg gaactgttaa actcctgata tactacacat caagattaca ctcaggagtc 180
117     ccatcaaagt tcagtggcag tgggtctgga acagattatt ctctcaccat tagcaacctg 240
118     gagcaagagg atattgccac ttacttttgc caacagggta atacgcttcc gtggacgttc 300
119     gctggaggca ccaagctgga aatcaaacgg gctggaggcg gtagtggcgg tggatcgggg 360
120     ggaggcagcg gtggcggatc tgaggtgcag ctccagcagt ctggacctga gctggtgaag 420
121     cctggagctt caatgaagat atcctgcaag gcttctggtt actcattcac tggctacacc 480
122     atgaactggg tgaagcagag tcatggaaag aaccttgagt ggatgggact tattaatcct 540
123     tacaaaggtg ttagtaccta caaccagaag ttcaaggaca aggccacatt aactgtagac 600
124     aagtcattca gcacagccta catggaactc ctcagttcga catctgagga ctctgcagtc 660
125     tattactgtg caagatcggg gtactacggt gatagtgact ggtacttcga tgtctggggc 720
126     gcagggacca cggtcaccgt ctctcaaaa gcttccggag gtcccaggag cggcagcctg 780
127     gccgcgctga ccgcgcacca ggcttgccac ctgccgctgg agactttcac ccgtcatcgc 840
128     cagccgcgcg gctgggaaca actggagcag tgcggctatc cgggtgcagcg gctgggtcgcc 900
129     ctctacctgg cggcgcgggt gtcgtggaac caggtcgacc aggtgatccg caacgccctg 960
130     gccagccccg gcagcggcgg cgacctgggc gaagcgatcc gcgagcagcc ggagcaggcc 1020
131     cgtctggccc tgacctggc cgccgccgag agcgcgcgct tcgtccggca gggcaccggc 1080
132     aacgacgagg ccggcgcggc caacggcccc gcggacagcg gcgacgcctt gctggagcgc 1140
133     aactatccca ctggcgcgga gttcctcggc gacggcggcg acgtcagctt cagcaccgcg 1200
134     ggcacgcaga actggacggt ggagcggtct ctccaggcgc accgccaaact ggaggagcgc 1260
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137     ggcgatccgg cgctggccta cggtacgcc caggaccagg aaccgcagcg acgcggccgg 1440
138     atccgcaacg gtgccctgct gcgggtctat gtgcgcgct cgagcctgcc gggcttctac 1500
139     cgcaccagcc tgacctggc cgccgcggag gcggcggggc aggtcgaacg gctgatcggc 1560
140     catccgctgc cgctgcgctt ggacgccatc accggccccg aggaggaagg cgggcgcctg 1620
141     gagaccattc tcggtgggcc gctggccgag cgcaccgtgg tgattccctc ggcgatcccc 1680
142     accgaccgcg gcaacgtcgg cggcgacctc gaccgtcca gcatccccga caaggaacag 1740
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144     aag

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145 <210> SEQ ID NO 3
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148 <213> ORGANISM: Pseudomonas aeruginosa
149 <400> SEQUENCE: 3
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153               20             25             30
154   Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
155           35             40             45
156   Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
157       50             55             60
158   Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
159       65             70             75             80
160   Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
161               85             90             95
162   Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
163           100            105            110
164   Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
165           115            120            125
166   Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
167       130            135            140
168   Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
169       145            150            155            160
170   Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
171               165            170            175
172   Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
173           180            185            190
174   Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
175       195            200            205
176   Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
177       210            215            220
178   Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
179       225            230            235            240
180   Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
181               245            250            255
182   Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
183           260            265            270
184   Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
185       275            280            285
186   Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
187       290            295            300
188   Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
189       305            310            315            320
190   Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
191               325            330            335
192   Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
193           340            345            350
194   Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val

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196 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
197          370          375          380
198 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
199          385          390          395          400
200 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
201          405          410          415
202 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
203          420          425          430
204 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
205          435          440          445
206 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
207          450          455          460
208 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
209          465          470          475          480
210 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
211          485          490          495
212 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
213          500          505          510
214 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
215          515          520          525
216 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
217          530          535          540
218 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
219          545          550          555          560
220 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
221          565          570          575
222 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
223          580          585          590
224 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
225          595          600          605
226 Arg Glu Asp Leu Lys
227          610
228 <210> SEQ ID NO 4
229 <211> LENGTH: 25
230 <212> TYPE: PRT
231 <213> ORGANISM: Pseudomonas aeruginosa
232 <400> SEQUENCE: 4
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236      20          25
237 <210> SEQ ID NO 5
238 <211> LENGTH: 16
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
